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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=1; day=25; hr=17; min=43; sec=12; ms=958;]

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Reviewer Comments:

SEQUENCE LISTING

<110> SHINTANI et al.

<120> MEDICINAL USE OF MIP-3a INHIBITOR AND METHOD OF SCREENING
BRAIN/NERVE CELL PROTECTIVE AGENT

The above <120> response exceeds the Sequence Rules' required 72-
character limit per line (this includes white spaces). Please insert a
hard return after "SCREENING."

<210> 5
<211> 291
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(291)
<223>

<220>
<221> sig_peptide
<222> (1)..(81)
<223>

<220>
<221> mat_peptide
<222> (82)..()

<223>

<400> 5

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Met Ala Cys Gly Gly Lys Arg Leu Leu Phe Leu Ala Leu Ala Trp Val	
-25 -20 -15	
ctg ctg gct cac ctc tgc agc cag gca gaa gca gca agc aac tac gac	96
Leu Leu Ala His Leu Cys Ser Gln Ala Glu Ala Ala Ser Asn Tyr Asp	
-10 -5 -1 1 5	
tgt tgc ctc tcg tac ata cag acg cct ctt cct tcc aga gct att gtg	144
Cys Cys Leu Ser Tyr Ile Gln Thr Pro Leu Pro Ser Arg Ala Ile Val	
10 15 20	
ggt ttc aca aga cag atg gcc gat gaa gct tgt gac att aat gct atc	192
Gly Phe Thr Arg Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile	
25 30 35	
atc ttt cac acg aag aaa aga aaa tct gtg tgc gct gat cca aag cag	240
Ile Phe His Thr Lys Lys Arg Lys Ser Val Cys Ala Asp Pro Lys Gln	
40 45 50	
aac tgg gtg aaa agg gct gtg aac ctc ctc agc cta aga gtc aag aag	288
Asn Trp Val Lys Arg Ala Val Asn Leu Leu Ser Leu Arg Val Lys Lys	
55 60 65	
atg	291
Met	

70 In the above last line, "70" is not properly aligned under "Met," the last amino acid. Same type of error in Sequence 7.

Application No: 10547532 Version No: 2.0

Input Set:

Output Set:

Started: 2008-01-17 13:20:25.407
 Finished: 2008-01-17 13:20:35.219
 Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 812 ms
 Total Warnings: 17
 Total Errors: 25
 No. of SeqIDs Defined: 21
 Actual SeqID Count: 21

Error code	Error Description
E 201	Mandatory field data missing in <223> in SEQ ID (1)
E 201	Mandatory field data missing in <223> in SEQ ID (1)
E 201	Mandatory field data missing in <223> in SEQ ID (1)
E 201	Mandatory field data missing in <223> in SEQ ID (3)
E 201	Mandatory field data missing in <223> in SEQ ID (3)
E 201	Mandatory field data missing in <223> in SEQ ID (3)
E 201	Mandatory field data missing in <223> in SEQ ID (5)
E 201	Mandatory field data missing in <223> in SEQ ID (5)
E 201	Mandatory field data missing in <223> in SEQ ID (5)
W 112	Upper case found in data; Found at position(291) SeqId(5)
E 259	Found undefined lettercode; POS (293) SEQID(5)
E 254	The total number of bases conflicts with running total, Input: 70, Calculated : 294 SEQID(5)
E 253	The number of bases differs from <211> Input: 291 Calculated:294
E 201	Mandatory field data missing in <223> in SEQ ID (7)
W 112	Upper case found in data; Found at position(1122) SeqId(7)
E 259	Found undefined lettercode; POS (1124) SEQID(7)
W 112	Upper case found in data; Found at position(1125) SeqId(7)
E 259	Found undefined lettercode; POS (1127) SEQID(7)
W 112	Upper case found in data; Found at position(1128) SeqId(7)

Input Set:

Output Set:

Started: 2008-01-17 13:20:25.407
Finished: 2008-01-17 13:20:35.219
Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 812 ms
Total Warnings: 17
Total Errors: 25
No. of SeqIDs Defined: 21
Actual SeqID Count: 21

Error code	Error Description
E 259	Found undefined lettercode; POS (1130) SEQID(7)
W 112	Upper case found in data; Found at position(1131) SeqId(7)
E 259	Found undefined lettercode; POS (1134) SEQID(7)
W 112	Upper case found in data; Found at position(1134) SeqId(7)
W 112	Upper case found in data; Found at position(1137) SeqId(7)
E 259	Found undefined lettercode; POS (1139) SEQID(7)
E 254	The total number of bases conflicts with running total, Input: 370, Calculated : 1140 SEQID(7)
E 253	The number of bases differs from <211> Input: 1122
E 201	Mandatory field data missing in <223> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
E 201	Mandatory field data missing in <223> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (15)
E 201	Mandatory field data missing in <223> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)

Input Set:

Output Set:

Started: 2008-01-17 13:20:25.407
Finished: 2008-01-17 13:20:35.219
Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 812 ms
Total Warnings: 17
Total Errors: 25
No. of SeqIDs Defined: 21
Actual SeqID Count: 21

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)

SEQUENCE LISTING

<110> SHINTANI et al.

<120> MEDICINAL USE OF MIP-3a INHIBITOR AND METHOD OF SCREENING BRAIN/NERVE CELL PROTECTIVE AGENT

<130> 20039.0001USWO

<140> 10547532

<141> 2008-01-17

<150> PCT/JP2004/002774

<151> 2004-03-04

<150> JP 2003-056885

<151> 2003-03-04

<150> JP 2003-106247

<151> 2003-04-10

<160> 21

<170> PatentIn version 3.1

<210> 1

<211> 288

<212> DNA

<213> Homo sapiens

<220>

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<222> (1)..(288)

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<221> sig_peptide

<222> (1)..(78)

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<221> mat_peptide

<222> (79)..()

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Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu	
-25 -20 -15	
cta ctc cac ctc tgc ggc gaa tca gaa gca gca agc aac ttt gac tgc	96
Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys	
-10 -5 -1 1 5	
tgt ctt gga tac aca gac cgt att ctt cat cct aaa ttt att gtg ggc	144
Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly	
10 15 20	
ttc aca cgg cag ctg gcc aat gaa ggc tgt gac atc aat gct atc atc	192

Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
25 30 35
ttt cac aca aag aaa aag ttg tct gtg tgc gca aat cca aaa cag act 240
Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
40 45 50
tgg gtg aaa tat att gtg cgt ctc ctc agt aaa aaa gtc aag aac atg 288
Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met
55 60 65 70

<210> 2
<211> 96
<212> PRT
<213> Homo sapiens

<400> 2
Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu
-25 -20 -15
Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys
-10 -5 -1 1 5
Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
10 15 20
Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
25 30 35
Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
40 45 50
Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met
55 60 65 70

<210> 3
<211> 288
<212> DNA
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<220>
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<222> (1)..(288)
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<221> sig_peptide
<222> (1)..(75)
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<220>
<221> mat_peptide
<222> (76)..()
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<400> 3
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-25 -20 -15 -10
gct tac ctc tgc agc cag tca gaa gca gca agc aac ttt gac tgc tgc 96
Ala Tyr Leu Cys Ser Gln Ser Glu Ala Ala Ser Asn Phe Asp Cys Cys
-5 -1 1 5
ctc acg tac aca aag aac gtg tat cat cat gcg aga aat ttt gtg ggt 144
Leu Thr Tyr Thr Lys Asn Val Tyr His His Ala Arg Asn Phe Val Gly

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      10              15              20
ttc aca aca cag atg gcc gac gaa gct tgt gac att aat gct atc atc      192
Phe Thr Thr Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile Ile
      25              30              35
ttt cac ctg aag tcg aaa aga tcc gtg tgc gct gac cca aag cag atc      240
Phe His Leu Lys Ser Lys Arg Ser Val Cys Ala Asp Pro Lys Gln Ile
      40              45              50              55
tgg gtg aaa agg att ttg cac ctc ctc agc cta aga acc aag aag atg      288
Trp Val Lys Arg Ile Leu His Leu Leu Ser Leu Arg Thr Lys Lys Met
              60              65              70

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<210> 4
<211> 96
<212> PRT
<213> Rattus norvegicus

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<400> 4
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-25              -20              -15              -10
Ala Tyr Leu Cys Ser Gln Ser Glu Ala Ala Ser Asn Phe Asp Cys Cys
              -5              -1 1              5
Leu Thr Tyr Thr Lys Asn Val Tyr His His Ala Arg Asn Phe Val Gly
      10              15              20
Phe Thr Thr Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile Ile
      25              30              35
Phe His Leu Lys Ser Lys Arg Ser Val Cys Ala Asp Pro Lys Gln Ile
      40              45              50              55
Trp Val Lys Arg Ile Leu His Leu Leu Ser Leu Arg Thr Lys Lys Met
              60              65              70

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<210> 5
<211> 291
<212> DNA
<213> Mus musculus

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<220>
<221> CDS
<222> (1)..(291)
<223>

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<220>
<221> sig_peptide
<222> (1)..(81)
<223>

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<220>
<221> mat_peptide
<222> (82)..()
<223>

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<400> 5
atg gcc tgc ggt ggc aag cgt ctg ctc ttc ctt gct ttg gca tgg gta      48
Met Ala Cys Gly Gly Lys Arg Leu Leu Phe Leu Ala Leu Ala Trp Val
      -25              -20              -15
ctg ctg gct cac ctc tgc agc cag gca gaa gca gca agc aac tac gac      96
Leu Leu Ala His Leu Cys Ser Gln Ala Glu Ala Ala Ser Asn Tyr Asp
      -10              -5              -1 1              5

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tgt tgc ctc tgc tac ata cag acg cct ctt cct tcc aga gct att gtg      144
Cys Cys Leu Ser Tyr Ile Gln Thr Pro Leu Pro Ser Arg Ala Ile Val
      10                      15                      20
ggg ttc aca aga cag atg gcc gat gaa gct tgt gac att aat gct atc      192
Gly Phe Thr Arg Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile
      25                      30                      35
atc ttt cac acg aag aaa aga aaa tct gtg tgc gct gat cca aag cag      240
Ile Phe His Thr Lys Lys Arg Lys Ser Val Cys Ala Asp Pro Lys Gln
      40                      45                      50
aac tgg gtg aaa agg gct gtg aac ctc ctc agc cta aga gtc aag aag      288
Asn Trp Val Lys Arg Ala Val Asn Leu Leu Ser Leu Arg Val Lys Lys
      55                      60                      65
atg                                                                291
Met                                                                70

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<210> 6
<211> 97
<212> PRT
<213> Mus musculus

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<400> 6
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      -10                      -5                      -1 1 5
Cys Cys Leu Ser Tyr Ile Gln Thr Pro Leu Pro Ser Arg Ala Ile Val
      10                      15                      20
Gly Phe Thr Arg Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile
      25                      30                      35
Ile Phe His Thr Lys Lys Arg Lys Ser Val Cys Ala Asp Pro Lys Gln
      40                      45                      50
Asn Trp Val Lys Arg Ala Val Asn Leu Leu Ser Leu Arg Val Lys Lys
      55                      60                      65
Met
70

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<210> 7
<211> 1122
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (1)..(1122)
<223>

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<400> 7
atg agc ggg gaa tca atg aat ttc agc gat gtt ttc gac tcc agt gaa      48
Met Ser Gly Glu Ser Met Asn Phe Ser Asp Val Phe Asp Ser Ser Glu
1 5 10 15
gat tat ttt gtg tca gtc aat act tca tat tac tca gtt gat tct gag      96
Asp Tyr Phe Val Ser Val Asn Thr Ser Tyr Tyr Ser Val Asp Ser Glu
20 25 30
atg tta ctg tgc tcc ttg cag gag gtc agg cag ttc tcc agg cta ttt      144
Met Leu Leu Cys Ser Leu Gln Glu Val Arg Gln Phe Ser Arg Leu Phe
35 40 45

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gta ccg att gcc tac tcc ttg atc tgt gtc ttt ggc ctc ctg ggg aat	192
Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly Asn	
50 55 60	
att ctg gtg gtg atc acc ttt gct ttt tat aag aag gcc agg tct atg	240
Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met	
65 70 75 80	
aca gac gtc tat ctc ttg aac atg gcc att gca gac atc ctc ttt gtt	288
Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val	
85 90 95	
ctt act ctc cca ttc tgg gca gtg agt cat gcc act ggt gcg tgg gtt	336
Leu Thr Leu Pro Phe Trp Ala Val Ser His Ala Thr Gly Ala Trp Val	
100 105 110	
ttc agc aat gcc acg tgc aag ttg cta aaa ggc atc tat gcc atc aac	384
Phe Ser Asn Ala Thr Cys Lys Leu Leu Lys Gly Ile Tyr Ala Ile Asn	
115 120 125	
ttt aac tgc ggg atg ctg ctc ctg act tgc att agc atg gac cgg tac	432
Phe Asn Cys Gly Met Leu Leu Leu Thr Cys Ile Ser Met Asp Arg Tyr	
130 135 140	
atc gcc att gta cag gcg act aag tca ttc cgg ctc cga tcc aga aca	480
Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg Thr	
145 150 155 160	
cta ccg cgc agc aaa atc atc tgc ctt gtt gtg tgg ggg ctg tca gtc	528
Leu Pro Arg Ser Lys Ile Ile Cys Leu Val Val Trp Gly Leu Ser Val	
165 170 175	
atc atc tcc agc tca act ttt gtc ttc aac caa aaa tac aac acc caa	576
Ile Ile Ser Ser Ser Thr Phe Val Phe Asn Gln Lys Tyr Asn Thr Gln	
180 185 190	
ggc agc gat gtc tgt gaa ccc aag tac cag act gtc tcg gag ccc atc	624
Gly Ser Asp Val Cys Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile	
195 200 205	
agg tgg aag ctg ctg atg ttg ggg ctt gag cta ctc ttt ggt ttc ttt	672
Arg Trp Lys Leu Leu Met Leu Gly Leu Glu Leu Leu Phe Gly Phe Phe	
210 215 220	
atc cct ttg atg ttc atg ata ttt tgt tac acg ttc att gtc aaa acc	720
Ile Pro Leu Met Phe Met Ile Phe Cys Tyr Thr Phe Ile Val Lys Thr	
225 230 235 240	
ttg gtg caa gct cag aat tct aaa agg cac aaa gcc atc cgt gta atc	768
Leu Val Gln Ala Gln Asn Ser Lys Arg His Lys Ala Ile Arg Val Ile	
245 250 255	
ata gct gtg gtg ctt gtg ttt ctg gct tgt cag att cct cat aac atg	816
Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met	
260 265 270	
gtc ctg ctt gtg acg gct gca aat ttg ggt aaa atg aac cga tcc tgc	864
Val Leu Leu Val Thr Ala Ala Asn Leu Gly Lys Met Asn Arg Ser Cys	
275 280 285	
cag agc gaa aag cta att ggc tat acg aaa act gtc aca gaa gtc ctg	912
Gln Ser Glu Lys Leu Ile Gly Tyr Thr Lys Thr Val Thr Glu Val Leu	
290 295 300	
gct ttc ctg cac tgc tgc ctg aac cct gtg ctc tac gct ttt att ggg	960
Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly	
305 310 315 320	
cag aag ttc aga aac tac ttt ctg aag atc ttg aag gac ctg tgg tgt	1008
Gln Lys Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu Trp Cys	
325 330 335	
gtg aga agg aag tac aag tcc tca ggc ttc tcc tgt gcc ggg agg tac	1056
Val Arg Arg Lys Tyr Lys Ser Ser Gly Phe Ser Cys Ala Gly Arg Tyr	
340 345 350	

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 gcg tcg tcc ttc act atg 1122
 Ala Ser Ser Phe Thr Met 370

<210> 8
 <211> 374
 <212> PRT
 <213> Homo sapiens

<400> 8
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 Met Leu Leu Cys Ser Leu Gln Glu Val Arg Gln Phe Ser Arg Leu Phe
 35 40 45
 Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly Asn
 50 55 60
 Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met
 65 70 75 80
 Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val
 85 90 95
 Leu Thr Leu Pro Phe Trp Ala Val Ser His Ala Thr Gly Ala Trp Val
 100 105 110
 Phe Ser Asn Ala Thr Cys Lys Leu Leu Lys Gly Ile Tyr Ala Ile Asn
 115 120 125
 Phe Asn Cys Gly Met Leu Leu Leu Thr Cys Ile Ser Met Asp Arg Tyr
 130 135 140
 Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg Thr
 145 150 155 160
 Leu Pro Arg Ser Lys Ile Ile Cys Leu Val Val Trp Gly Leu Ser Val
 165 170 175
 Ile Ile Ser Ser Ser Thr Phe Val Phe Asn Gln Lys Tyr Asn Thr Gln
 180 185 190
 Gly Ser Asp Val Cys Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile
 195 200 205
 Arg Trp Lys Leu Leu Met Leu Gly Leu Glu Leu Leu Phe Gly Phe Phe
 210 215 220
 Ile Pro Leu Met Phe Met Ile Phe Cys Tyr Thr Phe Ile Val Lys Thr
 225 230 235 240
 Leu Val Gln Ala Gln Asn Ser Lys Arg His Lys Ala Ile Arg Val Ile
 245 250 255
 Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met
 260 265 270
 Val Leu Leu Val Thr Ala Ala Asn Leu Gly Lys Met Asn Arg Ser Cys
 275 280 285
 Gln Ser Glu Lys Leu Ile Gly Tyr Thr Lys Thr Val Thr Glu Val Leu
 290 295 300
 Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly
 305 310 315 320
 Gln Lys Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu Trp Cys
 325 330 335
 Val Arg Arg Lys Tyr Lys Ser Ser Gly Phe Ser Cys Ala Gly Arg Tyr
 340 345 350

Ser Glu Asn Ile Ser Arg Gln Thr Ser Glu Thr Ala Asp Asn Asp Asn
 355 360 365
 Ala Ser Ser Phe Thr Met
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<210> 9
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 <212> DNA
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<220>
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 <222> (1)..(1101)
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<400> 9
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 gag tat tat tct att cct cca gac cat ggg cca tgc tcc cta gaa gag 96
 Glu Tyr Tyr Ser Ile Pro Pro Asp His Gly Pro Cys Ser Leu Glu Glu
 20 25 30
 gtc aga aac ttc acc aag gta ttt gtg cca att gcc tac tcc tta ata 144
 Val Arg Asn Phe Thr Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile
 35 40 45
 tgt gtc ttt ggc ctc ctg ggc aac att atg gtg gtg atg acc ttt gcc 192
 Cys Val Phe Gly Leu Leu Gly Asn Ile Met Val Val Met Thr Phe Ala
 50 55 60
 ttc tac aag aaa gcc aga tcc atg act gac gtc tac ctg ttg aac atg 240
 Phe Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met
 65 70 75 80
 gcc atc aca gac ata ctc ttt gtc ctc acc cta ccg ttc tgg gca gtt 288
 Ala Ile Thr